

U.S. DEPARTMENT OF COMMERCE PATENT & TRADEMARK OFFICE

<b>Transmittal Letter to the United States Designated/Elected Office (DO/EO/US) Concerning a Filing Under 35 USC 371</b>		<b>Attorney's Docket Number</b> <b>REF/FLUGGE/168</b>
		<b>U.S. Application Number</b> <b>09/719,168</b>
<b>International Application Number</b> <b>PCT/EP99/04095</b>	<b>International Filing Date</b> <b>June 14, 1999</b>	<b>Priority Date Claimed</b> <b>June 13, 1998</b>
<b>Title of Invention</b> <b>DNA SEQUENCES WHICH CODE A GLUCOSE-TRANSLOCATOR, PLASMIDS, BACERTIA, YEASTS AND PLANTS CONTAINING THIS TRANSLOCATOR</b>		
<b>Applicant(s) for DO/EO/US</b> <b>FLUGGE et al.</b>		

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items under 35 USC 371:

1. ☒ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 USC 371.
2. ☐ An oath or declaration of the inventor(s) (35 USC 371(c)(4)). (☐ Executed ☐ Unexecuted)
3. ☒ A copy of Form PCT/DO/EO/905 dated: April 30, 2001.
4. ☒ A Sequence Listing paper copy and a computer readable disk.
5. ☐ An assignment document for recording.  
A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
6. ☐ A **FIRST** preliminary amendment.  
☐ A **SECOND** or **SUBSEQUENT** preliminary amendment.
7. ☐ A substitute specification.
8. ☐ A change of power of attorney and/or address letter.
9. ☐ A Verified Statement Claiming Small Entity Status.
10. ☐ A Request for Refund.
11. ☐ Surcharge in the amount of \$ 0.00.
12. ☐ Assignment recordation fee of \$ 0.00.
13. ☐ Processing fee of \$ for furnishing the English translation later than ☐ 20 ☐ 30 months from the earliest claimed priority date (37 CFR 1.492(f)).

A check in the amount of \$ 0.00 to cover the fees is enclosed.

The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to **Deposit Account Number 02-0200**. A duplicate copy of this sheet is enclosed.

Respectfully submitted,  
BACON & THOMAS, PLLC

By: Richard E. Fichter  
RICHARD E. FICHTER  
Registration No. 26,382

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Date: July 30, 2001



JC20 Rec'd PCT/PTO 30 JUL 2001  
09/719168 PCT #3

PATENT

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

In re Application of:

SAWATZKI et al.

Serial No.: 09/719,168

Filed: December 13, 2000

For: DNA SEQUENCES WHICH CODE A GLUCOSE-TRANSLOCATOR,  
PLASMIDS, BACTERIA, YEASTS AND PLANTS CONTAINING  
THIS TRANSLOCATOR

Attention:

PCT BOX MISSING PARTS

**PETITION FOR EXTENSION OF TIME**

Assistant Commissioner for Patents  
Washington, D.C. 20231

Sir:

Applicants request that the period for response to the outstanding official action in this case be extended pursuant to 37 CFR 1.136 (a) for ONE (1) month to July 30, 2001.

The fee set in 37 CFR 1.17(a) for a one month extension of time is \$55.00 and a check in this amount is submitted herewith. Small entity status has been established. Please charge any additional fee required for this extension to Deposit Account No. 02-0200. A duplicate copy of this paper is attached.

Respectfully submitted,  
BACON & THOMAS, PLLC

By: Richard E. Fichter  
Richard E. Fichter  
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Facsimile: (703) 683-1080

REF:kdd  
EXT-SML.EX1.wpd

July 30, 2001

09/719168

PATENT

**IN THE UNITED STATES PATENT AND TRADEMARK OFFICE**

In re Application of:

SAWATZKI et al.

Serial No.: 09/719,168

Filed: December 13, 2000

For: DNA SEQUENCES WHICH CODE A GLUCOSE-TRANSLOCATOR,  
PLASMIDS, BACTERIA, YEASTS AND PLANTS CONTAINING  
THIS TRANSLOCATOR

Attention:

PCT BOX MISSING PARTS

**RESPONSE AND SUBMISSION OF MISSING PARTS OF APPLICATION**

Assistant Commissioner for Patents  
Washington, D.C. 20231

Sir:

This is in response to the Official Action dated April 30, 2001, in connection with the above-identified application which is a Notification of Missing Part Requirements with a period for response set to expire on June 30, 2001. The period for response has been extended to expire on July 30, 2001, by the filing herewith of a Petition for a One Month Extension of Time and payment of the appropriate fee for a small entity.


The Official Action states that Applicants must submit the required Sequence Listing as referred to on the attached form PCT/DO/EO/905 which states that Applicants must provide an initial or substitute computer readable form of the Sequence Listing and a statement that the content of the paper or compact disk and the computer readable form are the same and where applicable include no new matter.

Applicants most respectfully submit that the Sequence Listing contained on the computer disk submitted herewith corresponds to that contained in the specification of the present application as originally filed. No new matter has been introduced. A paper copy of the Sequence Listing contained on the computer readable disk submitted herewith is also submitted herewith.

In view of the above submission of an initial computer readable disk, application is now complete and it should be further processed and forwarded to the examining group for an examination on the merits.

Respectfully submitted,

BACON & THOMAS, PLLC

By:   
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Facsimile: 703-683-1080

REF/kdd  
MissPts PCT Ltr toPTO.wpd

July 30, 2001

09/719168

#3

DNA-sequences coding for a glucose-translocator, plasmids, bacteria, yeast  
and plants containing this transporter  
PCT/EP99/04095

Prof. Dr. Flügge, Ulf-Ingo

# SEQUENCE LISTING OF PLASTIDIC GLUCOSE TRANSPORTERS

Zea mays

1874 nucleotides

Coding region: nucleotides 2 to 1630

3'-untranslated region: nucleotides 1631 to 1874

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g gca cga gag atg atg cgc tgc gct gca acg ggc ggc ggg tgc gtc gct 49
Ala Arg Glu Met Met Arg Cys Ala Ala Thr Gly Gly Gly Cys Val Ala
  1         5         10        15
tcg tgg agc ggc gat cgg aga ttg ccg gcg gtc aac ccc tgc agc gtg 97
Ser Trp Ser Gly Asp Arg Arg Leu Pro Ala Val Asn Pro Cys Ser Val
  20        25        30
cgg atg ccg acg ggc aac gat ggg tgg tgc gcc ggc ctg agg tgc cgg 145
Arg Met Pro Thr Gly Asn Asp Gly Trp Cys Ala Gly Leu Arg Ser Arg
  35        40        45
gcg gcg gat ctc gcc ggc ctc gag atg gcc aac ctg cgc ggc ggc gtc 193
Ala Ala Asp Leu Ala Gly Leu Glu Met Ala Asn Leu Arg Gly Gly Val
  50        55        60
ggg ggg ctc ttc cgc gcg agc ccg cgc tac ggg cgc ttg caa gcc acg 241
Gly Gly Leu Phe Arg Ala Ser Pro Arg Tyr Gly Arg Leu Gln Ala Thr
  65        70        75        80
gcg gca gtt gac cct gaa gat att cca ttg gag aag gtt caa gtt aaa 289
Ala Ala Val Asp Pro Glu Asp Ile Pro Leu Glu Lys Val Gln Val Lys
  85        90        95
tcc tca gga cat gtt ctg cca tat gtt ggc gtt gct tgt ttg ggg gct 337
Ser Ser Gly His Val Leu Pro Tyr Val Gly Val Ala Cys Leu Gly Ala
 100       105       110
att ctg ttt ggt tac cat ctt ggt gtg gtc aat ggc gca ctt gaa tat 385
Ile Leu Phe Gly Tyr His Leu Gly Val Val Asn Gly Ala Leu Glu Tyr
 115       120       125
ctc gcg aag gat ctt ggg att gct gaa aat gct gtc ttg cag ggg tgg 433
Leu Ala Lys Asp Leu Gly Ile Ala Glu Asn Ala Val Leu Gln Gly Trp
 130       135       140
gtg gtt agc aca tcc ttg gct ggt gca aca cta ggt tct ttt act ggg 481
Val Val Ser Thr Ser Leu Ala Gly Ala Thr Leu Gly Ser Phe Thr Gly
 145       150       155       160
ggt tct ttg gca gat aaa ttt ggg cgg aca aga aca ttc atc ctg gat 529
Gly Ser Leu Ala Asp Lys Phe Gly Arg Thr Arg Thr Phe Ile Leu Asp
 165       170       175

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gca gtc cca ctt gct cta ggt gca ttc ttg agt gca aca gct caa gat 577  
Ala Val Pro Leu Ala Leu Gly Ala Phe Leu Ser Ala Thr Ala Gln Asp  
180 185 190  
atc cgc aca atg att att ggc cga ttg ctt gct gga att ggt atc ggg 625  
Ile Arg Thr Met Ile Ile Gly Arg Leu Leu Ala Gly Ile Gly Ile Gly  
195 200 205  
gtc tca tct gct ctt gta ccc ctt tac ata tct gag atc tca cca act 673  
Val Ser Ser Ala Leu Val Pro Leu Tyr Ile Ser Glu Ile Ser Pro Thr  
210 215 220  
gaa att cgt gga aca ctt ggt acc gtt aat caa ctt ttt att tgc att 721  
Glu Ile Arg Gly Thr Leu Gly Thr Val Asn Gln Leu Phe Ile Cys Ile  
225 230 235 240  
gga att ctt gca gct ttg tta gct gga ttg cct ctg gca gga aat cct 769  
Gly Ile Leu Ala Ala Leu Leu Ala Gly Leu Pro Leu Ala Gly Asn Pro  
245 250 255  
gcc tgg tgg agg aca atg ttt gga att gct gta gtt cca tcc att ctg 817  
Ala Trp Trp Arg Thr Met Phe Gly Ile Ala Val Val Pro Ser Ile Leu  
260 265 270  
ctg gct gta gga atg gcc ttt tcg cct gaa agc cct cgt tgg cta ttc 865  
Leu Ala Val Gly Met Ala Phe Ser Pro Glu Ser Pro Arg Trp Leu Phe  
275 280 285  
cag caa gga aag gtt act caa gca gaa tta gct gta aaa aga ctg tat 913  
Gln Gln Gly Lys Val Thr Gln Ala Glu Leu Ala Val Lys Arg Leu Tyr  
290 295 300  
gga aaa gaa atg gtt acc gaa att atg ttt gat ctg aga gct agt ggc 961  
Gly Lys Glu Met Val Thr Glu Ile Met Phe Asp Leu Arg Ala Ser Gly  
305 310 315 320  
caa agt tct tcg gag tcc gaa gcc ggc tgg ttt gat ctt ttc agc aag 1009  
Gln Ser Ser Ser Glu Ser Glu Ala Gly Trp Phe Asp Leu Phe Ser Lys  
325 330 335  
cgt tac tgg aaa gtt gtg agt gtg ggg gca gca ctg ttt ttg ttc cag 1057  
Arg Tyr Trp Lys Val Val Ser Val Gly Ala Ala Leu Phe Leu Phe Gln  
340 345 350  
cag ctt gct ggt ata aac gct gtt gta tat tac tct aca tcg gtg ttc 1105  
Gln Leu Ala Gly Ile Asn Ala Val Val Tyr Tyr Ser Thr Ser Val Phe  
355 360 365  
cgt agt gca ggc att gca tct gat gtt gct gct agt gct ctt gtt gga 1153  
Arg Ser Ala Gly Ile Ala Ser Asp Val Ala Ala Ser Ala Leu Val Gly  
370 375 380  
gca gcc aat gtt ttt ggt act atg gtt gca tct tct cta atg gac aaa 1201  
Ala Ala Asn Val Phe Gly Thr Met Val Ala Ser Ser Leu Met Asp Lys  
385 390 395 400  
caa gga agg aaa agc ctt ctg ata aca agc ttt tct gga atg ggt gct 1249  
Gln Gly Arg Lys Ser Leu Leu Ile Thr Ser Phe Ser Gly Met Gly Ala  
405 410 415  
tca atg cta ctc cta gca ttg tcc ttc acc tgg aaa gct ctg gca cct 1297

Ser Met Leu Leu Leu Ala Leu Ser Phe Thr Trp Lys Ala Leu Ala Pro  
 420 425 430  
 tat tct ggt act ctt gct gtt gtt ggc act gtt ctg tac gtg ctg tca 1345  
 Tyr Ser Gly Thr Leu Ala Val Val Gly Thr Val Leu Tyr Val Leu Ser  
 435 440 445  
 ttg gct cta gga gcg ggc cct gtt cca gcg cta ctt ctt cct gaa ata 1393  
 Phe Ala Leu Gly Ala Gly Pro Val Pro Ala Leu Leu Leu Pro Glu Ile  
 450 455 460  
 ttg gcc tcg aga ata agg gcc aag gct gtc gca tta tct cta ggc atg 1441  
 Phe Ala Ser Arg Ile Arg Ala Lys Ala Val Ala Leu Ser Leu Gly Met  
 465 470 475 480  
 cac tgg gta tct aac ttg ttc att ggc ctg tac ttc ctg agt gtc gtg 1489  
 His Trp Val Ser Asn Phe Phe Ile Gly Leu Tyr Phe Leu Ser Val Val  
 485 490 495  
 agc aag ttg ggg atc agc aac gtg tat ctg gga ttg gca tca gta tgt 1537  
 Ser Lys Phe Gly Ile Ser Asn Val Tyr Leu Gly Phe Ala Ser Val Cys  
 500 505 510  
 gcc ctt gca gtt ctg tac ata gct ggg aat gtg gtc gag acc aag ggg 1585  
 Ala Leu Ala Val Leu Tyr Ile Ala Gly Asn Val Val Glu Thr Lys Gly  
 515 520 525  
 aga tca ctt gaa gag att gaa agg gag cta agt gta gca gaa tga 1630  
 Arg Ser Leu Glu Glu Ile Glu Arg Glu Leu Ser Val Ala Glu  
 530 535 540  
 tgtacttttg ctagtcatgc tgtggcgccg ttgtggttat cgagaatgca accaagcgct 1690  
 caaccgagca tccttgacc tggagactct ttctagtttc atgtagtttt agaaataagc 1750  
 gaacggcaag agtaccatc ttaggtgact tgggtggtt tgtgtctgaa ataagtgaat 1810  
 tggattgtag aatttcagaa ataagtgaat tggattgtag aatttcaaaa aaaaaaaaaa 1870  
 aaaa 1874

# Solanum tuberosum

1653 nucleotides

Coding region: nucleotides 1 to 1419

3'-untranslated region: nucleotides 1420 to 1653

ggc cgc tgc aga tca cac aga gtt cga gct gct gga gag gat att gag 48  
 Gly Arg Cys Arg Ser His Arg Val Arg Ala Ala Gly Glu Asp Ile Glu  
 1 5 10 15  
 gat gca gca cct ctc aaa gtt caa ggc caa tca tct gga tca gta ctt 96  
 Asp Ala Ala Pro Leu Lys Val Gln Gly Gln Ser Ser Gly Ser Val Leu  
 20 25 30  
 ccc tat gtg ggt gta gct tgt ctg gga gca att tta ttg gga tat cac 144  
 Pro Tyr Val Gly Val Ala Cys Leu Gly Ala Ile Leu Phe Gly Tyr His  
 35 40 45  
 cta ggg gtg gtg aat ggt gcc ctt gag tac cta gct aag gat ctt gga 192  
 Leu Gly Val Val Asn Gly Ala Leu Glu Tyr Leu Ala Lys Asp Leu Gly

50                      55                      60  
 att gcc gag aac act gtt ata caa gga tgg att gtt agc aca gtt ctt 240  
 Ile Ala Glu Asn Thr Val Ile Gln Gly Trp Ile Val Ser Thr Val Leu  
 65                      70                      75                      80  
 gct ggc gcc ttt gtt ggt tca ttt act ggt gga gtt ctg gct gat aaa 288  
 Ala Gly Ala Phe Val Gly Ser Phe Thr Gly Gly Val Leu Ala Asp Lys  
 85                      90                      95  
 ttt ggc cga aca aag aca ttt ata ttg gat gca att cca ctt tca gtt 336  
 Phe Gly Arg Thr Lys Thr Phe Ile Leu Asp Ala Ile Pro Leu Ser Val  
 100                      105                      110  
 ggt gcg ttt cta tgt acc act gcc cag agt gtt cag gct atg atc att 384  
 Gly Ala Phe Leu Cys Thr Thr Ala Gln Ser Val Gln Ala Met Ile Ile  
 115                      120                      125  
 gga cgc tta ctt act gga att ggc att ggc atc tca tct gct att gtg 432  
 Gly Arg Leu Leu Thr Gly Ile Gly Ile Gly Ile Ser Ser Ala Ile Val  
 130                      135                      140  
 cca ctt tac ata tct gag atc tca ccc act gaa att cgc ggc aca ctg 480  
 Pro Leu Tyr Ile Ser Glu Ile Ser Pro Thr Glu Ile Arg Gly Thr Leu  
 145                      150                      155                      160  
 gga acg gtc aat cag cta ttc att tgc att gga att ctt gtt gca ctc 528  
 Gly Thr Val Asn Gln Leu Phe Ile Cys Ile Gly Ile Leu Val Ala Leu  
 165                      170                      175  
 gtg gtt gga ttg cct ttg tct gga aat cct tgc tgg tgg aga aca atg 576  
 Val Val Gly Leu Pro Leu Ser Gly Asn Pro Ser Trp Trp Arg Thr Met  
 180                      185                      190  
 ttt ggt ctc gca ctt att cca tct gtt tta ctt gca ata gga atg gca 624  
 Phe Gly Leu Ala Leu Ile Pro Ser Val Leu Leu Ala Ile Gly Met Ala  
 195                      200                      205  
 ttt tct cct gaa agt cct cgg tgg ctc tat cag caa ggg aga att tct 672  
 Phe Ser Pro Glu Ser Pro Arg Trp Leu Tyr Gln Gln Gly Arg Ile Ser  
 210                      215                      220  
 gaa gct gag aca tct att aaa agg cta tat ggt aaa gaa aaa gtt gct 720  
 Glu Ala Glu Thr Ser Ile Lys Arg Leu Tyr Gly Lys Glu Lys Val Ala  
 225                      230                      235                      240  
 gag gtt atg ggt gac ttg gaa gct tct gcc cgg ggt tct tca gaa cca 768  
 Glu Val Met Gly Asp Leu Glu Ala Ser Ala Arg Gly Ser Ser Glu Pro  
 245                      250                      255  
 gat gct ggg tgg ctt gat cta ttt agt agc cgt tat agg aaa gtt gtt 816  
 Asp Ala Gly Trp Leu Asp Leu Phe Ser Ser Arg Tyr Arg Lys Val Val  
 260                      265                      270  
 agc att ggt gca gct atg ttc ttg ttg cag cag ttg gct ggg ata aat 864  
 Ser Ile Gly Ala Ala Met Phe Leu Leu Gln Gln Leu Ala Gly Ile Asn  
 275                      280                      285  
 gct gtt gtc tat tat tcc act gcc gtg ttc cgg agt gct gga att aca 912  
 Ala Val Val Tyr Tyr Ser Thr Ala Val Phe Arg Ser Ala Gly Ile Thr  
 290                      295                      300



tct gat gta gca gcc agt gct ctg gtt gga gca gcc aac gtc ttt ggg 960  
Ser Asp Val Ala Ala Ser Ala Leu Val Gly Ala Ala Asn Val Phe Gly  
305 310 315 320  
aca acg gtg gca tcc tct ttg atg gac aaa caa gga agg aag agt ctc 1008  
Thr Thr Val Ala Ser Ser Leu Met Asp Lys Gln Gly Arg Lys Ser Leu  
325 330 335  
ttg ctc ata agc tat act gga atg gct gca tca atg atg ttg ctt tcc 1056  
Leu Leu Ile Ser Tyr Thr Gly Met Ala Ala Ser Met Met Leu Leu Ser  
340 345 350  
ttg tca ttc act tgg aag gtc ctg act cca tat tct ggc aca ctg gct 1104  
Leu Ser Phe Thr Trp Lys Val Leu Thr Pro Tyr Ser Gly Thr Leu Ala  
355 360 365  
ggt ctt ggt act gtc ctc tat gtg ttg tcc ttt tca ctt ggt gct ggt 1152  
Val Leu Gly Thr Val Leu Tyr Val Leu Ser Phe Ser Leu Gly Ala Gly  
370 375 380  
cct gtg cct gct ctt cta ctt cca gaa ata ttt gct tcc aga att agg 1200  
Pro Val Pro Ala Leu Leu Leu Pro Glu Ile Phe Ala Ser Arg Ile Arg  
385 390 395 400  
gca aaa gcg gtg gct ctc tct ttg ggg gta cat tgg ata atg aac ttc 1248  
Ala Lys Ala Val Ala Leu Ser Leu Gly Val His Trp Ile Met Asn Phe  
405 410 415  
ttt att ggc ctg tac ttc ttg agc att gta act aaa ttt ggt atc agt 1296  
Phe Ile Gly Leu Tyr Phe Leu Ser Ile Val Thr Lys Phe Gly Ile Ser  
420 425 430  
acg gtg tac atg gga ttt gca ctc tct tgt ctt gtt gct gtc gtg tat 1344  
Thr Val Tyr Met Gly Phe Ala Leu Ser Cys Leu Val Ala Val Val Tyr  
435 440 445  
ata act ggt aat gtc gtg gag aca aag ggg cgg tca ctg gag gag ata 1392  
Ile Thr Gly Asn Val Val Glu Thr Lys Gly Arg Ser Leu Glu Glu Ile  
450 455 460  
gaa cgt gag tta agt cca gca att tga gtggtacaac atgaacagct 1439  
Glu Arg Glu Leu Ser Pro Ala Ile  
465 470  
gagagtaatt tcagattccg ccatccagtg ggtcttgatt ttgaagagat tctccacatt 1499  
gggagttcta ttattgcgag actggagtgt catcacttac cctttagcta tctctttgat 1559  
ttctgttac gtcggcatca tgaatcatgg aacattgtaa aaacatgtaa ctgttatgga 1619  
agatgatccg cgtatgattg agtatttcaa aaaa 1653

*Spinacia oleracea*

1864 nucleotides

Coding region: nucleotides 61 to 1716

5'-untranslated region: nucleotides 1 to 60

3'-untranslated region: nucleotides 1717 to 1864

ggcacgaggc gatcgctgct taatcaattt caactttcgg ttagaaaaa gagggggaaa 60  
 atg cag gcg tca act ttt atg gtc aaa ggc aat ttg ggt ttt gaa gtt 108  
 Met Gln Ala Ser Thr Phe Met Val Lys Gly Asn Leu Gly Phe Glu Val  
 1 5 10 15  
 cag aac cgt aga gtg gct ggg ctt gct ggg ttg aaa ggg tta agc tca 156  
 Gln Asn Arg Arg Val Ala Gly Leu Ala Gly Leu Lys Gly Leu Ser Ser  
 20 25 30  
 atc cgt tcc aat aat cta agt ttt gtg aat gtt aat gac aat aat tat 204  
 Ile Arg Ser Asn Asn Leu Ser Phe Val Asn Val Asn Asp Asn Asn Tyr  
 35 40 45  
 aag tct aat ccc tgt aaa ttg agt tgt ggg tcc ctt tcg atg ggt gct 252  
 Lys Ser Asn Pro Cys Lys Leu Ser Cys Gly Ser Leu Ser Met Gly Ala  
 50 55 60  
 gga ttt gca aga ttg ggt ctt gat cat gtc atg aag tcc tca ccc aag 300  
 Gly Phe Ala Arg Leu Gly Leu Asp His Val Met Lys Ser Ser Pro Lys  
 65 70 75 80  
 tac aga tca gtc aag gct caa gct gct tct gga gga gat ctt gaa gat 348  
 Tyr Arg Ser Val Lys Ala Gln Ala Ala Ser Gly Gly Asp Leu Glu Asp  
 85 90 95  
 gcc act cct gtc aaa tat caa ggc aaa tct tct gca tca gtg ttg ccg 396  
 Ala Thr Pro Val Lys Tyr Gln Gly Lys Ser Ser Ala Ser Val Leu Pro  
 100 105 110  
 tat gtt ggt gtt gct tgt ttg gga gct att ttg ttt gga tat cac ctt 444  
 Tyr Val Gly Val Ala Cys Leu Gly Ala Ile Leu Phe Gly Tyr His Leu  
 115 120 125  
 ggt gtg gta aat gga gct ctt gac tac cta tct gcg gat tta gct att 492  
 Gly Val Val Asn Gly Ala Leu Asp Tyr Leu Ser Ala Asp Leu Ala Ile  
 130 135 140  
 gct ggc aat act gtt tta caa gga tgg gtt gtg agc ata tta ctt gct 540  
 Ala Gly Asn Thr Val Leu Gln Gly Trp Val Val Ser Ile Leu Leu Ala  
 145 150 155 160  
 gga gcg act gta ggt tca ttt act ggc gga tct ttg gct gat aag ttt 588  
 Gly Ala Thr Val Gly Ser Phe Thr Gly Gly Ser Leu Ala Asp Lys Phe  
 165 170 175  
 gga agg aca aag acc ttc cag tta gat gca att cct ctt gca ata gga 636  
 Gly Arg Thr Lys Thr Phe Gln Leu Asp Ala Ile Pro Leu Ala Ile Gly  
 180 185 190  
 gct tat ctc tgt gcc aca gca caa aat gta cag ata atg atg att ggt 684  
 Ala Tyr Leu Cys Ala Thr Ala Gln Asn Val Gln Ile Met Met Ile Gly  
 195 200 205  
 cgt tta ctt tgt ggc att gga att ggc ata tca tct gcc tta gtt ccg 732  
 Arg Leu Leu Cys Gly Ile Gly Ile Gly Ile Ser Ser Ala Leu Val Pro  
 210 215 220  
 tta tac att tct gag att tcg cca act gaa att cga ggt gca ctt ggt 780  
 Leu Tyr Ile Ser Glu Ile Ser Pro Thr Glu Ile Arg Gly Ala Leu Gly  
 225 230 235 240

tct gtc aac cag ctt ttt ata tgc att ggt att ctt gcg gct ttg gtt 828  
Ser Val Asn Gln Leu Phe Ile Cys Ile Gly Ile Leu Ala Ala Leu Val  
245 250 255  
gct gga ttg cct tta gca gga aac cct ttg tgg tgg agg aca atg ttt 876  
Ala Gly Leu Pro Leu Ala Gly Asn Pro Leu Trp Trp Arg Thr Met Phe  
260 265 270  
ggc att gca aca gtt ccc tct gtt ctc ttg gct ctt ggg atg ggc ttc 924  
Gly Ile Ala Thr Val Pro Ser Val Leu Leu Ala Leu Gly Met Gly Phe  
275 280 285  
tgt cca gaa agc cct agg tgg ctt ttt cag caa gga aaa att gtt gaa 972  
Cys Pro Glu Ser Pro Arg Trp Leu Phe Gln Gln Gly Lys Ile Val Glu  
290 295 300  
gca gaa aag gcc gta gca gcc ctc tat gga aaa gaa agg gtt ccg gag 1020  
Ala Glu Lys Ala Val Ala Ala Leu Tyr Gly Lys Glu Arg Val Pro Glu  
305 310 315 320  
gtg att aat gat ttg aga gca tct gtt caa ggt tct tct gaa cca gaa 1068  
Val Ile Asn Asp Leu Arg Ala Ser Val Gln Gly Ser Ser Glu Pro Glu  
325 330 335  
gct ggc tgg ttt gat ctg ttc agt agc cgc tac agg aaa gtg gta agt 1116  
Ala Gly Trp Phe Asp Leu Phe Ser Ser Arg Tyr Arg Lys Val Val Ser  
340 345 350  
gtt ggt gct gca ctt ttc ttg ttc cag caa atg gca gga atc aat gct 1164  
Val Gly Ala Ala Leu Phe Leu Phe Gln Gln Met Ala Gly Ile Asn Ala  
355 360 365  
gtt gta tat tac tcc aca tct gta ttc cga agt gct gga att gca tca 1212  
Val Val Tyr Tyr Ser Thr Ser Val Phe Arg Ser Ala Gly Ile Ala Ser  
370 375 380  
gat gtt gcc gct agt gcc ctt gtt gga gca tca aat gtt att ggc act 1260  
Asp Val Ala Ala Ser Ala Leu Val Gly Ala Ser Asn Val Ile Gly Thr  
385 390 395 400  
gct gtc gcc tct tct tta atg gac aag caa gga aga aag agc cta ctg 1308  
Ala Val Ala Ser Ser Leu Met Asp Lys Gln Gly Arg Lys Ser Leu Leu  
405 410 415  
atg aca agt ttc tca gga atg gct gcc tca atg ttg ttg ctg tca cta 1356  
Met Thr Ser Phe Ser Gly Met Ala Ala Ser Met Leu Leu Leu Ser Leu  
420 425 430  
tcg ttc aca tgg aag gct cta gca cct tac tcg ggc aca ctt gcc gtt 1404  
Ser Phe Thr Trp Lys Ala Leu Ala Pro Tyr Ser Gly Thr Leu Ala Val  
435 440 445  
gtg gga act gtt tta tat gtc ctt tcc ttt tca ctt ggc gct ggt cct 1452  
Val Gly Thr Val Leu Tyr Val Leu Ser Phe Ser Leu Gly Ala Gly Pro  
450 455 460  
gtt cct gct ctt cta ctt cca gag atc ttc gca tcc aga atc cga gca 1500  
Val Pro Ala Leu Leu Leu Pro Glu Ile Phe Ala Ser Arg Ile Arg Ala  
465 470 475 480  
aaa gca gtg gct ttg tca ctg gga atg cat tgg gcg tca aac ttc gta 1548

Lys Ala Val Ala Leu Ser Leu Gly Met His Trp Ala Ser Asn Phe Val  
           485                  490                  495  
 att ggc ctt tat ttc tta agt gtg gtg acc aag ttt gga atc agc aaa 1596  
 Ile Gly Leu Tyr Phe Leu Ser Val Val Thr Lys Phe Gly Ile Ser Lys  
           500                  505                  510  
 gtg tat ttg ggg ttc gcg tca gtg tgt gtg ctt gcc gtg ttg tac ata 1644  
 Val Tyr Leu Gly Phe Ala Ser Val Cys Val Leu Ala Val Leu Tyr Ile  
           515                  520                  525  
 gct ggt aac gtt gtt gaa aca aaa gga cga tca ctt gag gaa ata gag 1692  
 Ala Gly Asn Val Val Glu Thr Lys Gly Arg Ser Leu Glu Glu Ile Glu  
           530                  535                  540  
 ctt gct cta agt cca gct gtt tag ttggaggat acagttttc tgttttttg 1746  
 Leu Ala Leu Ser Pro Ala Val  
 545                  550  
 atctatagag aattatgta ataattcccg gatttaggag ttgatgcta gtttcatgc 1806  
 attcatgtcc agacagttgt actatcaatg tcagaaattc ctcggtgcc 1864